

**Figure 1 : Alignment of the BASB040 polynucleotide sequences.
Identity to SeqID No:1 is indicated by a dot.**

	* 20 *	
Seqid1 :	ATGATGATCAAACCGACCGCCCTGCTCCTG	: 30
Seqid3 :	: 30
Seqid5 :		: -
	40 * 60	
Seqid1 :	CCGGCTTATTTCCTTCCGCACGCATAC	: 60
Seqid3 :	: 60
Seqid5 :		: -
	* 80 *	
Seqid1 :	GCGCCTGCCGCCGACCTTCCGAAAACAAG	: 90
Seqid3 :	: 90
Seqid5 :	: 24
	100 * 120	
Seqid1 :	GCGGCGGGTTTCGCATTGTTAAAAACAAA	: 120
Seqid3 :	: 120
Seqid5 :	: 54
	* 140 *	
Seqid1 :	AGCCCCGACACCGAATCAGTTAAATTAAAA	: 150
Seqid3 :	: 150
Seqid5 :C.....	: 84
	160 * 180	
Seqid1 :	CCCAAATTCCCCGTCCGCATCGACACGCAG	: 180
Seqid3 :	: 180
Seqid5 :T.....	: 114

* 200 *

Seqid1 :	GATAGTCAAAGATATGGTCGAAGAA	:	210
Seqid3 :	:	210
Seqid5 :	..C.....	:	144

220 * 240

Seqid1 :	CACCTGCCGCTCATCACGCAGCAGCAGGAA	:	240
Seqid3 :	:	240
Seqid5 :	:	174

* 260 *

Seqid1 :	GAAGTATTGGACAAGGAACAGACGGGCTTC	:	270
Seqid3 :	:	270
Seqid5 :	:	204

280 * 300

Seqid1 :	CTCGCCGAAGAACGCACCGGACAACGTTAAA	:	300
Seqid3 :	:	300
Seqid5 :G.....	:	234

* 320 *

Seqid1 :	ACCATGCTCCGCAGCAAAGGCTATTCAGC	:	330
Seqid3 :	:	330
Seqid5 :	..G.....	:	264

340 * 360

Seqid1 :	AGCAAAGTCAGCCTGACGGAAAAAGACGGA	:	360
Seqid3 :	:	360
Seqid5 :	:	294

Seqid1 : GCTTATACGGTACACATCACACCGGGCCCG : 390
Seqid3 : : 390
Seqid5 : : 324

400 * 420
Seqid1 : CGCACCAAAATGCCAACGTCGGTGTGCC : 420
Seqid3 : : 420
Seqid5 :C.... : 354

* 440 *
Seqid1 : ATCCTCGCGACATCCTTCAGACGGCAAC : 450
Seqid3 : : 450
Seqid5 : : 384

460 * 480
Seqid1 : CTCGCCGAATACTACCGCAACGCGCTGGAA : 480
Seqid3 : : 480
Seqid5 : : 414

* 500 *
Seqid1 : AACTGGCAGCAGCCGGTAGGCAGTGATTTC : 510
Seqid3 : : 510
Seqid5 :C.... : 444

520 * 540
Seqid1 : GATCAGGACAGTTGGAAAACAGCAAAACT : 540
Seqid3 : : 540
Seqid5 : : 474

* 560 *
Seqid1 : TCCGTCTCGCGCGGTAAACGCGAAAAGGC : 570
Seqid3 :C.... : 570

Seqid5 :C....C. : 504

580 * 600
Seqid1 : TACCCGCTTGC~~A~~AGCTCGGCAACACCCGG : 600
Seqid3 : : 600
Seqid5 :T..G.A. : 534

* 620 *
Seqid1 : GCGGCCGTCAACCCCGATACC~~G~~CCACCGTC : 630
Seqid3 : : 630
Seqid5 :C. : 564

640 * 660
Seqid1 : GATTGAA~~C~~GT~~C~~GTGGACAGCGGCCGC : 660
Seqid3 : : 660
Seqid5 : : 594

* 680 *
Seqid1 : CCCATCGCCTTCGGCGACTTTGAAATCACC : 690
Seqid3 : : 690
Seqid5 : : 624

700 * 720
Seqid1 : GGCACACAGCGTTACCCCGAACAAATCGTC : 720
Seqid3 : : 720
Seqid5 : : 654

* 740 *
Seqid1 : TCCGGCCTGGCGCGCTTCCAACC~~G~~GGCACG : 750
Seqid3 : : 750
Seqid5 :T....T....G..C..T..T.. : 684

	760	*	780	
Seqid1 :	CCCTACGACCTCGACCTGCTGCTCGACTTC	:	780	
Seqid3 :	:	780	
Seqid5 :	..G.....	:	714	

	*	800	*	
Seqid1 :	CAACAGGCACTCGAACAAAACGGGCATTAT	:	810	
Seqid3 :	:	810	
Seqid5 :G.....	:	744	

	820	*	840	
Seqid1 :	TCCGGCGCGTCCGTACAAGCCGACTTCGAC	:	840	
Seqid3 :	:	840	
Seqid5 :	:	774	

	*	860	*	
Seqid1 :	CGTCTCCAAGGCGACCGCGTCCCCGTCAAA	:	870	
Seqid3 :	:	870	
Seqid5 :	..C.....	:	804	

	880	*	900	
Seqid1 :	GTCAGCGTAACCGAGGTCAAACGCCACAAG	:	900	
Seqid3 :	:	900	
Seqid5 :A	:	834	

	*	920	*	
Seqid1 :	CTCGAAACCGGCATCCGCCTCGATTGGAA	:	930	
Seqid3 :	:	930	
Seqid5 :	:	864	

	940	*	960	
Seqid1 :	TACGGTTGGCGGGAAAATCGCCTACGAC	:	960	

Seqid3 : : 960
Seqid5 : : 894

	*	980	*	
Seqid1	:	TATTACAACCTCTTCAACAAAGGCTATATC	:	990
Seqid3	:,.....	:	990
Seqid5	:	:	924

	1000	*	1020
Seqid1	: GGCTCGGT CGTCTGGGATATGGACAAATAC	:	1020
Seqid3	:	:	1020
Seqid5	: ..T.....	:	954

	1060	*	1080
Seqid1 :	CCGCGCAACTATCGGGGCAACTACTGGACA	:	1080
Seqid3 :	:	1080
Seqid5 :	:	1014

	*	1100	*	
Seqid1	:	AGCAACGTTCTACAAACCGTTGACCACC	:	1110
Seqid3	:	:	1110
Seqid5	:	:	1044

	1120	*	1140
Seqid1 :	CAAAACCTCGAAAAACGCGCCTTCTCCGGC	:	1140
Seqid3 :	:	1140
Seqid5 :	:	1074

* 1160 *

Seqid1 : GGCATCTGGTATGTGCGCGACCGCGCGGGC : 1170
Seqid3 : : 1170
Seqid5 : ...G..... : 1104

1180 * 1200

Seqid1 : ATCGATGCCAGGCTGGGGGCAGAGTTCTC : 1200
Seqid3 : : 1200
Seqid5 :G..A..... : 1134

* 1220 *

Seqid1 : GCAGAAGGCCGGAAAATCCCCGGCTCGGAT : 1230
Seqid3 : : 1230
Seqid5 :C. : 1164

1240 * 1260

Seqid1 : ATCGATTTGGGCAACAGCCACGCCACGATG : 1260
Seqid3 : : 1260
Seqid5 : G..... : 1194

* 1280 *

Seqid1 : CTGACCGCCTCTTGGAAACGCCAGCTGCTC : 1290
Seqid3 : : 1290
Seqid5 : : 1224

1300 * 1320

Seqid1 : AACAACGTGCTGCATCCGAAAACGGCCAT : 1320
Seqid3 : : 1320
Seqid5 : : 1254

* 1340 *

Seqid1 : TACCTCGACGGAAAATCGGTACGACTTG : 1350
Seqid3 : : 1350
Seqid5 : : 1284

1360 * 1380
Seqid1 : GGCACATTCTGTCCCTCCACCGCGCTGATC : 1380
Seqid3 : : 1380
Seqid5 : : 1314

* 1400 *
Seqid1 : CGCACCTCTGCCCGTGCAGGTTATTCCTTC : 1410
Seqid3 : : 1410
Seqid5 : : 1344

1420 * 1440
Seqid1 : ACGCCCGAAAACAAAAAACTCGGCACGTTC : 1440
Seqid3 : : 1440
Seqid5 : : 1374

* 1460 *
Seqid1 : ATCATACCGGACAAGCGGGTTACACCGTT : 1470
Seqid3 : : 1470
Seqid5 : : 1404

1480 * 1500
Seqid1 : GCCCGCGACAATGCCGACGTTCCCTCAGGG : 1500
Seqid3 : : 1500
Seqid5 : : 1434

* 1520 *
Seqid1 : CTGATGTTCCGCAGCGGGCGCGTCTTCC : 1530
Seqid3 : : 1530

Seqid5 : : 1464

1540 * 1560
Seqid1 : GTGCGCGGTTACGAACTCGACAGCATCGGA : 1560
Seqid3 : : 1560
Seqid5 : : 1494

* 1580 *
Seqid1 : CTTGCCGGCCCGAACGGATCGGTCTGCC : 1590
Seqid3 : : 1590
Seqid5 : : 1524

1600 * 1620
Seqid1 : GAACGCGCCCTCCTGGTGGCAGCCTGGAA : 1620
Seqid3 : : 1620
Seqid5 : : 1554

* 1640 *
Seqid1 : TACCAACTGCCGTTACGCGCACCCCTTCC : 1650
Seqid3 : : 1650
Seqid5 : : 1584

1660 * 1680
Seqid1 : GGCGCGGTGTTCCACGATATGGCGATGCC : 1680
Seqid3 : : 1680
Seqid5 : : 1614

* 1700 *
Seqid1 : GCCGCCAATTCAAACGTATGAAGCTGAAA : 1710
Seqid3 : : 1710
Seqid5 : : 1644

1720 * 1740
Seqid1 : CACGGTTCGGGACTGGCGTGCGCTGGTTC : 1740
Seqid3 : : 1740
Seqid5 : : 1674

* 1760 *
Seqid1 : AGCCCGCTTGCGCCGTTTCCTTCGACATC : 1770
Seqid3 : : 1770
Seqid5 : : 1704

1780 * 1800
Seqid1 : GCCTACGGGCACAGCGATAAGAAAATCCGC : 1800
Seqid3 : : 1800
Seqid5 : : 1734

* 1820 *
Seqid1 : TGGCACATCAGCTTGGGAACACGCTTCTAA : 1830
Seqid3 : : 1830
Seqid5 : : 1764

Figure 2 : Alignment of the BASB040 polypeptide sequences.
Identity to SeqID No:2 is indicated by a dot.

	*	20	*
Seqid2 :	MMIKPTALLLPALFFFPHAYAPAADLSENK	:	30
Seqid4 :	:	30
Seqid6 :	:	8

40 * 60
Seqid2 : AAGFALFKNKSPDTESVKLKPFPVRIDTQ : 60
Seqid4 : : 60
Seqid6 :L... : 38

* 80 *

Seqid2 : DSEIKDMVEEHLPLITQQQEEVLDKEQTGF : 90
Seqid4 : : 90
Seqid6 : : 68

100 * 120
Seqid2 : LAEEAPDNVKTMLRSKGYFSSKVSLTEKDG : 120
Seqid4 : : 120
Seqid6 : : 98

* 140 *

Seqid2 : AYTGHITPGPRTKIANVGAILGDIISDGN : 150
Seqid4 : : 150
Seqid6 : : 128

160 * 180

Seqid2 : LAEYYRNALENWQQPVGSDFDQDSWENSKT : 180
Seqid4 : : 180
Seqid6 : : 158

* 200 *

Seqid2 : SVLGAVTRKGYPLAKLGNTRAADVNPDTATV : 210
Seqid4 : : 210
Seqid6 :A.....Q.....A : 188

220 * 240

Seqid2 : DLNVVVDSGRPIAFGDFEITGTQRYPEQIV : 240
Seqid4 : : 240
Seqid6 : : 218

* 260 *

Seqid2 : SGLARFQPGTPYDLDLLLDFQQALEQNGHY : 270

Seqid4 : : 270

Seqid6 :M..... : 248

280 * 300

Seqid2 : SGASVQADFDRLQGDRVVKVSVTEVKRHK : 300

Seqid4 : : 300

Seqid6 : : 278

* 320 *

Seqid2 : LETGIRLDSEYGLGGKIAKYDYYNLFNKGYI : 330

Seqid4 : : 330

Seqid6 : : 308

340 * 360

Seqid2 : GSVVWDMDKYETTLAAGISQPRNYRGNYWT : 360

Seqid4 : : 360

Seqid6 : : 338

* 380 *

Seqid2 : SNVSYNRSTTQNLEKRAFSGGIWYVRDRAG : 390

Seqid4 : : 390

Seqid6 : : 368

400 * 420

Seqid2 : IDARLGAEFLAEGRKIPGSDIDLGNSHATM : 420

Seqid4 : : 420

Seqid6 :A..... : 398

* 440 *

Seqid2 : LTASWKRQLLNNVLHPENGHYLDGKIGTTL : 450

Seqid4 : : 450

Seqid6 : : 428

460 * 480

Seqid2 : GTFLSSTALIRTSARAGYFFT PENKKGTF : 480

Seqid4 : : 480

Seqid6 : : 458

* 500 *

Seqid2 : IIRGQAGYTVARDNADVPSGLMFRSGGASS : 510

Seqid4 : : 510

Seqid6 : : 488

520 * 540

Seqid2 : VRGYELDSIGLAGPNGSVLPERALLVGSLE : 540
Seqid4 : : 540
Seqid6 : : 518

* 560 *

Seqid2 : YQLPFTRTLSGAVFHDMDGDAANFKRMKLK : 570
Seqid4 : : 570
Seqid6 : : 548

580 * 600

Seqid2 : HGSGLGVRWFSP LAPFSFDIAYGHSDKKIR : 600
Seqid4 : : 600
Seqid6 : : 578

Seqid2 : WHISLGTRF : 609
Seqid4 : : 609
Seqid6 : : 587

SEQUENCE LISTING

<110> SmithKline Beecham Biologicals S.A.

<120> Novel compounds

<130> BM45339

<160> 11

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1830

<212> DNA

<213> *Neisseria meningitidis*

<400> 1

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gatagtaaaa tcaaagatat ggtcgaagaa caccctgcgc tcatcacgca	gcagcaggaa	240
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ctgatgttcc gcagcggcgg	cgcgtttcc gtgegcgggtt	acgaactcga cagcatcgga	1560
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gcccggcaatt tcaaacgtat	gaagctgaaa cacgggttcgg	gactgggcgt gcgctggttc	1740
agcccgcttg cgccgttttc	cttcgacatc gcctacgggc	acagcgataa gaaaatccgc	1800
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<210> 2

<211> 609

<212> PRT

<213> *Neisseria meningitidis*

<400> 2

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Pro His Ala Tyr Ala Pro Ala Ala Asp Leu Ser Glu Asn Lys Ala Ala			
20	25	30	
Gly Phe Ala Leu Phe Lys Asn Lys Ser Pro Asp Thr Glu Ser Val Lys			
35	40	45	
Leu Lys Pro Lys Phe Pro Val Arg Ile Asp Thr Gln Asp Ser Glu Ile			
50	55	60	
Lys Asp Met Val Glu Glu His. Leu Pro Leu Ile Thr Gln Gln Gln Glu			
65	70	75	80
Glu Val Leu Asp Lys Glu Gln Thr Gly Phe Leu Ala Glu Glu Ala Pro			
85	90	95	
Asp Asn Val Lys Thr Met Leu Arg Ser Lys Gly Tyr Phe Ser Ser Lys			
100	105	110	
Val Ser Leu Thr Glu Lys Asp Gly Ala Tyr Thr Val His Ile Thr Pro			
115	120	125	
Gly Pro Arg Thr Lys Ile Ala Asn Val Gly Val Ala Ile Leu Gly Asp			
130	135	140	
Ile Leu Ser Asp Gly Asn Leu Ala Glu Tyr Tyr Arg Asn Ala Leu Glu			
145	150	155	160
Asn Trp Gln Gln Pro Val Gly Ser Asp Phe Asp Gln Asp Ser Trp Glu			
165	170	175	
Asn Ser Lys Thr Ser Val Leu Gly Ala Val Thr Arg Lys Gly Tyr Pro			
180	185	190	
Leu Ala Lys Leu Gly Asn Thr Arg Ala Ala Val Asn Pro Asp Thr Ala			

195	200	205
Thr Val Asp Leu Asn Val Val Val Asp Ser Gly Arg Pro Ile Ala Phe		
210	215	220
Gly Asp Phe Glu Ile Thr Gly Thr Gln Arg Tyr Pro Glu Gln Ile Val		
225	230	235
Ser Gly Leu Ala Arg Phe Gln Pro Gly Thr Pro Tyr Asp Leu Asp Leu		
245	250	255
Leu Leu Asp Phe Gln Gln Ala Leu Glu Gln Asn Gly His Tyr Ser Gly		
260	265	270
Ala Ser Val Gln Ala Asp Phe Asp Arg Leu Gln Gly Asp Arg Val Pro		
275	280	285
Val Lys Val Ser Val Thr Glu Val Lys Arg His Lys Leu Glu Thr Gly		
290	295	300
Ile Arg Leu Asp Ser Glu Tyr Gly Leu Gly Gly Lys Ile Ala Tyr Asp		
305	310	315
Tyr Tyr Asn Leu Phe Asn Lys Gly Tyr Ile Gly Ser Val Val Trp Asp		
325	330	335
Met Asp Lys Tyr Glu Thr Thr Leu Ala Ala Gly Ile Ser Gln Pro Arg		
340	345	350
Asn Tyr Arg Gly Asn Tyr Trp Thr Ser Asn Val Ser Tyr Asn Arg Ser		
355	360	365
Thr Thr Gln Asn Leu Glu Lys Arg Ala Phe Ser Gly Gly Ile Trp Tyr		
370	375	380
Val Arg Asp Arg Ala Gly Ile Asp Ala Arg Leu Gly Ala Glu Phe Leu		
385	390	395
Ala Glu Gly Arg Lys Ile Pro Gly Ser Asp Ile Asp Leu Gly Asn Ser		
405	410	415
His Ala Thr Met Leu Thr Ala Ser Trp Lys Arg Gln Leu Leu Asn Asn		
420	425	430
Val Leu His Pro Glu Asn Gly His Tyr Leu Asp Gly Lys Ile Gly Thr		
435	440	445
Thr Leu Gly Thr Phe Leu Ser Ser Thr Ala Leu Ile Arg Thr Ser Ala		
450	455	460
Arg Ala Gly Tyr Phe Phe Thr Pro Glu Asn Lys Lys Leu Gly Thr Phe		
465	470	475
Ile Ile Arg Gly Gln Ala Gly Tyr Thr Val Ala Arg Asp Asn Ala Asp		
485	490	495
Val Pro Ser Gly Leu Met Phe Arg Ser Gly Gly Ala Ser Ser Val Arg		
500	505	510
Gly Tyr Glu Leu Asp Ser Ile Gly Leu Ala Gly Pro Asn Gly Ser Val		
515	520	525

Leu Pro Glu Arg Ala Leu Leu Val Gly Ser Leu Glu Tyr Gln Leu Pro
 530 535 540
 Phe Thr Arg Thr Leu Ser Gly Ala Val Phe His Asp Met Gly Asp Ala
 545 550 555 560
 Ala Ala Asn Phe Lys Arg Met Lys Leu Lys His Gly Ser Gly Leu Gly
 565 570 575
 Val Arg Trp Phe Ser Pro Leu Ala Pro Phe Ser Phe Asp Ile Ala Tyr
 580 585 590
 Gly His Ser Asp Lys Lys Ile Arg Trp His Ile Ser Leu Gly Thr Arg
 595 600 605
 Phe

<210> 3
 <211> 1830
 <212> DNA
 <213> *Neisseria meningitidis*

<400> 3

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gccgccaatt tcaaacgtat	gaagctggaaa cacggttcgg	gactgggcgt gcgcgtggttc	1740
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<210> 4

<211> 609

<212> PRT

<213> *Neisseria meningitidis*

<400> 4

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20	25	30	
Gly Phe Ala Leu Phe Lys Asn Lys Ser Pro Asp Thr Glu Ser Val Lys			
35	40	45	
Leu Lys Pro Lys Phe Pro Val Arg Ile Asp Thr Gln Asp Ser Glu Ile			
50	55	60	
Lys Asp Met Val Glu Glu His Leu Pro Leu Ile Thr Gln Gln Gln Glu			
65	70	75	80
Glu Val Leu Asp Lys Glu Gln Thr Gly Phe Leu Ala Glu Glu Ala Pro			
85	90	95	
Asp Asn Val Lys Thr Met Leu Arg Ser Lys Gly Tyr Phe Ser Ser Lys			
100	105	110	
Val Ser Leu Thr Glu Lys Asp Gly Ala Tyr Thr Val His Ile Thr Pro			
115	120	125	
Gly Pro Arg Thr Lys Ile Ala Asn Val Gly Val Ala Ile Leu Gly Asp			
130	135	140	
Ile Leu Ser Asp Gly Asn Leu Ala Glu Tyr Tyr Arg Asn Ala Leu Glu			
145	150	155	160
Asn Trp Gln Gln Pro Val Gly Ser Asp Phe Asp Gln Asp Ser Trp Glu			
165	170	175	
Asn Ser Lys Thr Ser Val Leu Gly Ala Val Thr Arg Lys Gly Tyr Pro			
180	185	190	
Leu Ala Lys Leu Gly Asn Thr Arg Ala Ala Val Asn Pro Asp Thr Ala			

195	200	205
Thr Val Asp Leu Asn Val Val Val Asp Ser Gly Arg Pro Ile Ala Phe		
210	215	220
Gly Asp Phe Glu Ile Thr Gly Thr Gln Arg Tyr Pro Glu Gln Ile Val		
225	230	235
Ser Gly Leu Ala Arg Phe Gln Pro Gly Thr Pro Tyr Asp Leu Asp Leu		
245	250	255
Leu Leu Asp Phe Gln Gln Ala Leu Glu Gln Asn Gly His Tyr Ser Gly		
260	265	270
Ala Ser Val Gln Ala Asp Phe Asp Arg Leu Gln Gly Asp Arg Val Pro		
275	280	285
Val Lys Val Ser Val Thr Glu Val Lys Arg His Lys Leu Glu Thr Gly		
290	295	300
Ile Arg Leu Asp Ser Glu Tyr Gly Leu Gly Gly Lys Ile Ala Tyr Asp		
305	310	315
Tyr Tyr Asn Leu Phe Asn Lys Gly Tyr Ile Gly Ser Val Val Trp Asp		
325	330	335
Met Asp Lys Tyr Glu Thr Thr Leu Ala Ala Gly Ile Ser Gln Pro Arg		
340	345	350
Asn Tyr Arg Gly Asn Tyr Trp Thr Ser Asn Val Ser Tyr Asn Arg Ser		
355	360	365
Thr Thr Gln Asn Leu Glu Lys Arg Ala Phe Ser Gly Gly Ile Trp Tyr		
370	375	380
Val Arg Asp Arg Ala Gly Ile Asp Ala Arg Leu Gly Ala Glu Phe Leu		
385	390	395
Ala Glu Gly Arg Lys Ile Pro Gly Ser Asp Ile Asp Leu Gly Asn Ser		
405	410	415
His Ala Thr Met Leu Thr Ala Ser Trp Lys Arg Gln Leu Leu Asn Asn		
420	425	430
Val Leu His Pro Glu Asn Gly His Tyr Leu Asp Gly Lys Ile Gly Thr		
435	440	445
Thr Leu Gly Thr Phe Leu Ser Ser Thr Ala Leu Ile Arg Thr Ser Ala		
450	455	460
Arg Ala Gly Tyr Phe Phe Thr Pro Glu Asn Lys Lys Leu Gly Thr Phe		
465	470	475
Ile Ile Arg Gly Gln Ala Gly Tyr Thr Val Ala Arg Asp Asn Ala Asp		
485	490	495
Val Pro Ser Gly Leu Met Phe Arg Ser Gly Gly Ala Ser Ser Val Arg		
500	505	510
Gly Tyr Glu Leu Asp Ser Ile Gly Leu Ala Gly Pro Asn Gly Ser Val		
515	520	525

Leu Pro Glu Arg Ala Leu Leu Val Gly Ser Leu Glu Tyr Gln Leu Pro
 530 535 540
 Phe Thr Arg Thr Leu Ser Gly Ala Val Phe His Asp Met Gly Asp Ala
 545 550 555 560
 Ala Ala Asn Phe Lys Arg Met Lys Leu Lys His Gly Ser Gly Leu Gly
 565 570 575
 Val Arg Trp Phe Ser Pro Leu Ala Pro Phe Ser Phe Asp Ile Ala Tyr
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 Gly His Ser Asp Lys Lys Ile Arg Trp His Ile Ser Leu Gly Thr Arg
 595 600 605
 Phe

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 <211> 1764
 <212> DNA
 <213> *Neisseria meningitidis*

<400> 5

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ctccgcagca	aaggctattt	cagcagcaaa	gtcagcctga	cggaaaaaga	cggagcttat	300
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ggcgacatcc	tttcagacgg	caacctcgcc	gaatactacc	gcaacgcgt	ggaaaaactgg	420
cagcagccgg	taggcagcga	tttcgatcag	gacagttggg	aaaacagcaa	aacttccgtc	480
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gtttcttaca	accgttcgac	cacccaaaac	ctcgaaaaac	gcgccttc	cgccggcg	1080
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<212> PRT

<213> *Neisseria meningitidis*

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Asn	Lys	Ser	Pro	Asp	Thr	Glu	Ser	Val	Lys	Leu	Lys	Pro	Lys	Phe	Pro
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Val	Leu	Ile	Asp	Thr	Gln	Asp	Ser	Glu	Ile	Lys	Asp	Met	Val	Glu	Glu
								35				40		45	
His	Leu	Pro	Leu	Ile	Thr	Gln	Gln	Gln	Glu	Glu	Val	Leu	Asp	Lys	Glu
								50				55		60	
Gln	Thr	Gly	Phe	Leu	Ala	Glu	Glu	Ala	Pro	Asp	Asn	Val	Lys	Thr	Met
								65				70		80	
Leu	Arg	Ser	Lys	Gly	Tyr	Phe	Ser	Ser	Lys	Val	Ser	Leu	Thr	Glu	Lys
								85				90		95	
Asp	Gly	Ala	Tyr	Thr	Val	His	Ile	Thr	Pro	Gly	Pro	Arg	Thr	Lys	Ile
								100				105		110	
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								115				120		125	
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Gly	Ser	Asp	Phe	Asp	Gln	Asp	Ser	Trp	Glu	Asn	Ser	Lys	Thr	Ser	Val
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Leu	Gly	Ala	Val	Thr	Arg	Lys	Ala	Tyr	Pro	Leu	Ala	Lys	Leu	Gly	Asn
								165				170		175	
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Val	Val	Asp	Ser	Gly	Arg	Pro	Ile	Ala	Phe	Gly	Asp	Phe	Glu	Ile	Thr
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Gln Pro Gly Met Pro Tyr Asp Leu Asp Leu Leu Asp Phe Gln Gln
225 230 235 240
Ala Leu Glu Gln Asn Gly His Tyr Ser Gly Ala Ser Val Gln Ala Asp
245 250 255
Phe Asp Arg Leu Gln Gly Asp Arg Val Pro Val Lys Val Ser Val Thr
260 265 270
Glu Val Lys Arg His Lys Leu Glu Thr Gly Ile Arg Leu Asp Ser Glu
275 280 285
Tyr Gly Leu Gly Gly Lys Ile Ala Tyr Asp Tyr Tyr Asn Leu Phe Asn
290 295 300
Lys Gly Tyr Ile Gly Ser Val Val Trp Asp Met Asp Lys Tyr Glu Thr
305 310 315 320
Thr Leu Ala Ala Gly Ile Ser Gln Pro Arg Asn Tyr Arg Gly Asn Tyr
325 330 335
Trp Thr Ser Asn Val Ser Tyr Asn Arg Ser Thr Thr Gln Asn Leu Glu
340 345 350
Lys Arg Ala Phe Ser Gly Gly Val Trp Tyr Val Arg Asp Arg Ala Gly
355 360 365
Ile Asp Ala Arg Leu Gly Ala Glu Phe Leu Ala Glu Gly Arg Lys Ile
370 375 380
Pro Gly Ser Ala Val Asp Leu Gly Asn Ser His Ala Thr Met Leu Thr
385 390 395 400
Ala Ser Trp Lys Arg Gln Leu Leu Asn Asn Val Leu His Pro Glu Asn
405 410 415
Gly His Tyr Leu Asp Gly Lys Ile Gly Thr Thr Leu Gly Thr Phe Leu
420 425 430
Ser Ser Thr Ala Leu Ile Arg Thr Ser Ala Arg Ala Gly Tyr Phe Phe
435 440 445
Thr Pro Glu Asn Lys Lys Leu Gly Thr Phe Ile Ile Arg Gly Gln Ala
450 455 460
Gly Tyr Thr Val Ala Arg Asp Asn Ala Asp Val Pro Ser Gly Leu Met
465 470 475 480
Phe Arg Ser Gly Gly Ala Ser Ser Val Arg Gly Tyr Glu Leu Asp Ser
485 490 495
Ile Gly Leu Ala Gly Pro Asn Gly Ser Val Leu Pro Glu Arg Ala Leu
500 505 510
Leu Val Gly Ser Leu Glu Tyr Gln Leu Pro Phe Thr Arg Thr Leu Ser
515 520 525
Gly Ala Val Phe His Asp Met Gly Asp Ala Ala Asn Phe Lys Arg

530 535 540
Met Lys Leu Lys His Gly Ser Gly Leu Gly Val Arg Trp Phe Ser Pro
545 550 555 560
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565 570 575
Ile Arg Trp His Ile Ser Leu Gly Thr Arg Phe
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<220>
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<400> 7

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20

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<400> 8

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21

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29

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<213> *Neisseria meningitidis*

<400> 11

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gccaaaacaa tgtgcgtcgg gaaaaccata cccgcgtatga cggcggtcag ggctgcggaa	300
aacgtaccaa tgaggtaaag gatgataatc ggcctgatata gtcgccttgcgtt gccttttgg	360
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